OM protein - protein search, using sw model

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Run on: August 9, 2006, 15:43:08 ; Search time 33 Seconds
(without alignments)
34.676 Million cell updates/sec

Title: US-10-810-919-4
Perfect score: 93
Sequence: 1 VHHQKLPFFAEDVGSNK 17
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 239914

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :
Published Applications AA New:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	84	90.3	28	7	US-11-297-316-2	Sequence 2, Appli
2	84	90.3	32	1	US-09-731-899-6	Sequence 6, Appli
3	84	90.3	40	1	US-09-731-899-8	Sequence 2, Appli
4	84	90.3	40	1	US-09-731-899-5	Sequence 5, Appli
5	84	90.3	40	7	US-11-104-300-3	Sequence 3, Appli
6	84	90.3	40	7	US-11-269-857-3	Sequence 3, Appli
7	84	90.3	42	1	US-09-731-899-3	Sequence 3, Appl
8	84	90.3	42	6	US-10-890-071-42	Sequence 42, Appl
9	84	90.3	42	1	US-11-104-300-2	Sequence 2, Appl
10	84	90.3	42	7	US-11-269-857-5	Sequence 5, Appl
11	84	90.3	42	7	US-11-297-316-5	Sequence 5, Appli
12	84	90.3	42	7	US-11-287-157A-49	Sequence 49, Appli
13	84	90.3	43	1	US-09-731-899-4	Sequence 4, Appli
14	84	90.3	58	7	US-10-515-919A-30	Sequence 30, Appl
15	84	90.3	59	1	US-09-731-899-1	Sequence 1, Appl
16	84	90.3	695	1	US-10-515-919A-8	Sequence 8, Appli
17	84	90.3	42	6	US-10-515-919A-3	Sequence 3, Appli
18	84	90.3	42	6	US-10-515-919A-13	Sequence 13, Appli
19	84	90.3	42	6	US-10-515-919A-18	Sequence 18, Appli
20	84	90.3	626	6	US-10-515-919A-5	Sequence 5, Appli
21	84	90.3	626	6	US-10-515-919A-1	Sequence 1, Appl
22	84	90.3	626	6	US-10-515-919A-2	Sequence 2, Appli
23	78	83.9	626	6	US-10-515-919A-17	Sequence 17, Appli
24	78	83.9	626	6	US-10-515-919A-12	Sequence 12, Appli
25	77	82.8	42	6	US-10-515-919A-4	Sequence 4, Appli
26	77	82.8	42	6	US-10-515-919A-6	Sequence 6, Appli
27	77	82.8	42	6	US-10-515-919A-9	Sequence 9, Appli
28	77	82.8	42	6	US-10-515-919A-11	Sequence 11, Appli
29	77	82.8	626	6	US-10-515-919A-14	Sequence 14, Appli
30	77	82.8	626	6	US-10-515-919A-16	Sequence 16, Appli
31	77	82.8	626	6	US-10-515-919A-19	Sequence 19, Appli
32	77	82.8	626	6	US-10-515-919A-21	Sequence 21, Appl
33	76	82.8	42	6	US-10-515-919A-22	Sequence 22, Appli
34	76	81.7	43	6	US-10-515-919A-23	Sequence 23, Appli
35	76	81.7	626	1	US-10-890-071-75	Sequence 75, Appli
36	73	78.5	19	6	US-10-890-071-27	Sequence 27, Appli
37	73	78.4	626	6	US-10-890-071-21	Sequence 21, Appli
38	72	77.4	770	7	US-10-890-071-75	Sequence 75, Appli
39	73	78.5	42	6	US-10-890-071-20	Sequence 20, Appli
40	72	77.4	626	6	US-10-890-071-27	Sequence 27, Appli
41	72	77.4	626	6	US-10-890-071-22	Sequence 22, Appli
42	52	55.9	42	6	US-10-890-071-26	Sequence 26, Appli
43	49	52.7	43	6	US-10-890-071-28	Sequence 28, Appli
44	48	51.6	626	6	US-10-890-071-28	Sequence 28, Appli
45	47	50.5	10	6	US-10-890-071-24	Sequence 24, Appli
46	46	49.5	10	6	US-10-890-071-23	Sequence 23, Appli
47	47	50.5	10	6	US-10-890-071-26	Sequence 26, Appli
48	44	47.3	10	6	US-10-890-071-29	Sequence 29, Appli
49	44	47.3	10	6	US-10-890-071-24	Sequence 24, Appli
50	43	46.2	10	6	US-10-890-071-23	Sequence 23, Appli
51	43	46.2	10	6	US-10-890-071-25	Sequence 25, Appli
52	41	44.1	163	6	US-10-953-349-20393	Sequence 20393, Appli
53	41	44.1	241	6	US-10-953-349-20392	Sequence 20392, Appli
54	41	44.1	290	6	US-10-953-349-23889	Sequence 23889, A
55	41	44.1	312	6	US-10-953-349-23888	Sequence 23888, A
56	41	44.1	376	6	US-10-953-349-23887	Sequence 23887, A
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61	40	43.0	517	7	US-11-056-355B-5191	Sequence 5191, A
62	40	43.0	517	7	US-11-056-355B-14652	Sequence 14652, A
63	40	43.0	517	7	US-11-056-355B-15358	Sequence 15358, A
64	40	43.0	538	7	US-11-056-355B-5190	Sequence 5190, Ap
65	40	43.0	538	7	US-11-056-355B-14651	Sequence 14651, A
66	40	43.0	538	7	US-11-056-355B-15357	Sequence 15357, A
67	40	43.0	458	7	US-10-953-349-24604	Sequence 24604, A
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69	39.5	42.5	464	7	US-11-056-355B-24603	Sequence 24603, A
70	39.5	42.5	464	7	US-10-953-349-24603	Sequence 24603, A
71	39.5	42.5	464	7	US-11-056-355B-53517	Sequence 53517, Ap
72	39.5	42.5	517	7	US-10-953-349-24602	Sequence 24602, A
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76	39	41.9	485	7	US-11-056-355B-32539	Sequence 32539, A
77	39	41.9	446	7	US-10-953-349-35425	Sequence 35425, A
78	39	41.9	492	7	US-10-953-349-3586	Sequence 3586, Ap
79	39	41.9	259	6	US-11-056-355B-28950	Sequence 28950, Ap
80	39	41.9	277	7	US-11-056-355B-32540	Sequence 32540, A
81	39	41.9	277	7	US-11-056-355B-86891	Sequence 86891, A
82	39	41.9	277	7	US-11-056-355B-19101	Sequence 19101, A
83	39	41.9	277	7	US-11-056-355B-71622	Sequence 71622, A
84	39	41.9	357	6	US-11-056-355B-71623	Sequence 71623, A
85	39	41.9	446	7	US-11-056-355B-19101	Sequence 19101, A
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92	39	41.9	572	7	US-11-056-355B-71621	Sequence 71621, A
93	39	41.9	618	7	US-11-056-355B-71383	Sequence 71383, A
94	39	41.9	702	6	US-10-540-898-341	Sequence 341, App
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121	38	40.9	130	7	US-10-471-571A-2390	Sequence 2390, Ap
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154	36	38.7	230	6	US-10-449-902-33278	Sequence 33278, A
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160	36	38.7	239	7	US-11-056-355B-37589	Sequence 37589, A
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163	36	38.7	239	7	US-11-056-355B-111237	Sequence 111237,
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165	36	38.7	240	7	US-11-056-355B-29179	Sequence 29179, A
166	36	38.7	240	7	US-11-056-355B-32769	Sequence 32769, A
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168	36	38.7	275	7	US-11-056-355B-111236	Sequence 111236,
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177	36	38.7	320	7	US-11-056-355B-99996	Sequence 99996, A
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183	36	38.7	326	7	US-11-330-403-13941	Sequence 13941, A
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185	36	38.7	348	7	US-11-283-329-60	Sequence 60, Appl
186	36	38.7	360	7	US-11-330-403-13968	Sequence 13968, A
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233	35	37.6	168	6	US-11-056-355B-83100	Sequence 83100, A
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235	35	37.6	168	7	US-11-056-355B-99998	Sequence 99998, A
236	35	37.6	168	7	US-11-056-355B-47401	Sequence 47401, A
237	35	37.6	168	7	US-11-056-355B-49675	Sequence 49675, A
238	35	37.6	171	7	US-10-953-349-8872	Sequence 8872, Ap
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241	35	37.6	171	7	US-11-056-355B-47400	Sequence 47400, A
242	35	37.6	183	6	US-11-056-355B-49674	Sequence 49674, A
243	35	37.6	183	7	US-10-449-902-47678	Sequence 47678, A
244	35	37.6	191	7	US-11-056-355B-83098	Sequence 83098, A

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Run on: August 9, 2006, 15:42:02 ; Search time 183 Seconds
(without alignments)
43.031 Million cell updates/sec

Title: US-10-810-919-4
Perfect score: 93
Sequence: 1 VHHQKLPFFAEDVGSNK. 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 46321858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
listing first 1000 summaries

Database : Published Applications AA Main:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	84	90.3	17	4	US-10-475-281-8	Sequence 8, Appli
4	84	90.3	17	4	US-10-810-919-3	Sequence 3, Appli
5	84	90.3	17	5	US-10-684-346-24	Sequence 24, Appl
6	84	90.3	17	5	US-10-997-078-46	Sequence 46, Appl
7	84	90.3	17	5	US-10-997-700-19	Sequence 19, Appl
8	84	90.3	17	6	US-11-066-697-950	Sequence 950, App
9	84	90.3	17	6	US-11-066-697-983	Sequence 983, App
10	84	90.3	24	5	US-10-728-246-5	Sequence 5, Appli
11	84	90.3	24	6	US-11-030-300-5	Sequence 5, Appli
12	84	90.3	28	3	US-09-867-847-4	Sequence 4, Appli
13	84	90.3	28	4	US-09-865-294-66	Sequence 66, Appl
14	84	90.3	28	3	US-09-792-079-5	Sequence 5, Appli
15	84	90.3	28	4	US-10-159-279-5	Sequence 5, Appli
16	84	90.3	28	4	US-10-363-082-2	Sequence 2, Appli
17	84	90.3	28	4	US-10-433-385-7	Sequence 7, Appli
18	84	90.3	28	4	US-10-390-472-4	Sequence 4, Appli
19	84	90.3	28	4	US-10-741-205-36	Sequence 36, Appl
20	84	90.3	28	4	US-10-416-262B-7	Sequence 7, Appli
21	84	90.3	28	4	US-10-478-308-4	Sequence 4, Appli
22	84	90.3	28	4	US-10-478-307-4	Sequence 4, Appli
23	84	90.3	28	5	US-10-861-614-66	Sequence 66, Appl
24	84	90.3	28	5	US-10-825-958-4	Sequence 4, Appli
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26	84	90.3	28	6	US-11-066-697-959	Sequence 959, App
27	84	90.3	28	6	US-11-066-697-965	Sequence 965, App
28	84	90.3	28	6	US-11-066-697-976	Sequence 976, App
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36	84	90.3	30	6	US-10-732-862A-98	Sequence 98, Appl
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OM protein - protein search, using sw model

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Run on: August 9, 2006, 15:41:44

Title: US-10-810-919-4
Perfect score: 93
Sequence: 1 VHHQKLPFFAEDVGSNK 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database : Issued_Patents_AA:*
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Search time 50 Seconds
(without alignments)
29,760 Million cell updates/sec

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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3	84	90.3	17	2	US-09-623-548A-983	Sequence 983, App
4	84	90.3	17	2	US-09-657-276-950	Sequence 950, App
5	84	90.3	17	2	US-09-657-276-983	Sequence 983, App
6	84	90.3	26	1	US-08-304-585-7	Sequence 7, Appli
7	84	90.3	28	1	US-08-346-849-4	Sequence 4, Appli
8	84	90.3	28	1	US-08-302-808-7	Sequence 7, Appli
9	84	90.3	28	1	US-08-609-090-2	Sequence 2, Appli
10	84	90.3	28	1	US-08-609-090-7	Sequence 7, Appli
11	84	90.3	28	1	US-08-986-948-7	Sequence 7, Appli
12	84	90.3	28	1	US-08-461-216-2	Sequence 2, Appli
13	84	90.3	28	1	US-08-293-284A-4	Sequence 4, Appli
14	84	90.3	28	2	US-09-388-890-3	Sequence 3, Appli
15	84	90.3	28	2	US-09-388-890-5	Sequence 5, Appli
16	84	90.3	28	2	US-09-388-890-6	Sequence 6, Appli
17	84	90.3	28	2	US-09-388-890-7	Sequence 7, Appli
18	84	90.3	28	2	US-09-388-890-8	Sequence 8, Appli
19	84	90.3	28	2	US-09-264-709A-1	Sequence 1, Appli
20	84	90.3	28	2	US-08-723-661B-2	Sequence 2, Appli
21	84	90.3	28	2	US-09-660-954-2	Sequence 2, Appli
22	84	90.3	28	2	US-09-660-954-3	Sequence 3, Appli
23	84	90.3	28	2	US-09-660-954-4	Sequence 4, Appli
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27	84	90.3	28	2	US-09-660-954-7	Sequence 7, Appli
28	84	90.3	28	2	US-09-660-954-8	Sequence 8, Appli
29	84	90.3	28	2	US-08-898-300-4	Sequence 4, Appli
30	84	90.3	28	2	US-08-824-513-4	Sequence 4, Appli
31	84	90.3	28	2	US-09-865-294A-66	Sequence 66, Appl
32	84	90.3	28	2	US-09-623-548A-965	Sequence 965, App
33	84	90.3	28	2	US-09-623-548A-976	Sequence 976, App
34	84	90.3	28	2	US-09-623-548A-992	Sequence 992, App
35	84	90.3	28	2	US-09-623-548A-1003	Sequence 1003, Ap
36	84	90.3	28	2	US-09-657-276-1003	Sequence 1003, Ap
37	84	90.3	28	2	US-09-657-276-992	Sequence 992, App
38	84	90.3	28	2	US-09-657-276-976	Sequence 976, App
39	84	90.3	28	1	US-10-363-082-2	Sequence 2, Appli
40	84	90.3	28	2	US-09-865-294A-66	Sequence 66, Appl
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58	84	90.3	39	2	US-09-657-276-1002	Sequence 1002, Ap
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62	84	90.3	39	1	US-08-682-245A-1	Sequence 1, Appli
63	84	90.3	39	1	US-08-304-585A-1	Sequence 1, Appli
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66	84	90.3	40	2	US-08-476-464A-2	Sequence 2, Appli
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78	84	90.3	40	3	US-09-062-365-3	Sequence 3, Appli
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108	84	90.3	1	US-08-302-808-5	Sequence 5, Appl
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152	84	90.3	34	US-09-979-952-34	Sequence 34, Appl
153	84	90.3	37	US-09-585-817-34	Sequence 37, Appl
154	84	90.3	20	US-09-962-955D-37	Sequence 20, Appl
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176	84	90.3	1	US-08-475-579A-1	Sequence 1, Appli
177	84	90.3	1	US-08-850-392-1	Sequence 1, Appli
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217	84	90.3	4	US-09-623-548A-987	Sequence 987, App
218	84	90.3	45	US-09-865-294A-70	Sequence 10, Appl
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220	84	90.3	48	US-09-560-883-1	Sequence 1, Appli
221	84	90.3	52	US-09-865-294A-74	Sequence 74, Appl
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233	84	90.3	67	US-09-027-292-1	Sequence 1, Appli
234	84	90.3	70	US-09-155-076-14	Sequence 14, Appl
235	84	90.3	82	US-09-848-616-173	Sequence 173, App
236	84	90.3	97	187153-8	Sequence 10, Appl
237	84	90.3	97	187153-8	Sequence 173, App
238	84	90.3	97	520013-8	Patent No. 187153
239	84	90.3	99	523482-8	Sequence 8, Appli
240	84	90.3	99	US-08-339-708A-4	Sequence 4, Appli
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242	84	90.3	100	US-08-422-333-3	Sequence 3, Appli
243	84	90.3	100	518153-10	Patent No. 518153
244	84	90.3	100	520013-10	Patent No. 520013
245	84	90.3	103	523482-10	Patent No. 523482

OM protein - protein search, using sw model

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Run on: August 9, 2006, 15:32:27 ; Search time 299 Seconds
(without alignments)
52.593 Million cell updates/sec

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Perfect score: 93
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Searched: 2849598 seqs, 925015592 residues
Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt 7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	84	90.3	42	2	Q7M088_CAVPO	cavia porce	
5	84	90.3	52	2	Q8WZ99_HUMAN	homo sapien	
6	84	90.3	52	2	Q29149_HUMAN	homo sapien	
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8	84	90.3	58	1	A4_CANFA	c amyloid b	
9	84	90.3	58	1	A4_RABIT	o amyloid b	
10	84	90.3	59	1	A4_SHEEP	o amyloid b	
11	84	90.3	58	1	A4_BOVIN	b amyloid b	
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22	84	90.3	751	2	Q95241_STECO	s amyloid b	
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33	84	90.3	770	1	A4_PIG	s amyloid b	
34	84	90.3	770	2	Q56JK6_CANFA	canis famil	
35	84	90.3	770	2	Q6RH30_CANFA	canis famil	
36	84	90.3	780	1	A4_TETFL	tetraodon f	
37	84	90.3	693	2	Q98SG0_XENLA	xenopus lae	
38	84	90.3	747	2	Q91963_9PIPI	xenopus. ap	
39	84	90.3	749	2	Q98SF9_XENLA	xenopus lae	
40	80	86.0	750	2	Q6DJB6_XENTR	xenopus tro	
41	80	86.0	695	2	Q6NRL1_XENLA	xenopus lae	
42	80	86.0	79	2	Q72XQ0_XENLA	xenopus lae	
43	77	82.8	218	2	Q35463_CRIGR	cricetulus	
44	76	81.7	384	2	Q8BPV5_MOUSE	mus musculu	
45	76	81.7	695	2	Q8BPC7_MOUSE	mus musculu	
46	76	81.7	695	2	Q6GR78_MOUSE	mus musculu	
47	76	81.7	733	2	Q6P6Q5_RAT	rattus norv	
48	76	81.7	752	2	Q6P6G5_RAT	rattus norv	
49	76	81.7	752	1	Q3TX19_MOUSE	mus musculu	
50	76	81.7	770	1	A4_MOUSE	m amyloid b	
51	76	81.7	770	1	A4_RAT	r amyloid b	
52	76	81.7	770	2	Q53ZT3_MOUSE	mus musculu	
53	76	81.7	64	2	Q3MQ25_ANTST	antechinus	
54	75	80.6	699	2	Q57394_NARJA	narke japon	
55	75	80.6	737	1	A4_FUGRU	fugu rubrip	
56	75	80.6	759	2	Q45O34_TETNG	tetraodon n	
57	75	80.6	357	2	Q8UUI8_BRARE	brachydanio	
58	72	77.4	472	2	Q8UUS0_BRARE	brachydanio	
59	72	77.4	612	2	Q8UU8O_BRARE	brachydanio	
60	72	77.4	678	2	Q7ZZT1_BRARE	brachydanio	
61	72	77.4	738	2	Q6NUZI_BRARE	brachydanio	
62	72	77.4	738	2	Q91987_BRARE	brachydanio	
63	72	77.4	738	2	Q90W28_BRARE	brachydanio	
64	55	59.9	49	2	Q97917_BOVIN	bos taurus	
65	52	55.9	49	2	Q2XQ98_PIG	sus scrofa	
66	51	54.8	239	2	Q8L5Y7_ARATH	arabidopsis	
67	51	54.8	362	2	Q8LS77_ARATH	arabidopsis	
68	51	54.8	694	2	Q9M1K5_ARATH	arabidopsis	
69	48	51.6	738	2	Q6SDL4_ROMMI	romalea mic	
70	48	51.6	475	2	Q8IYU3_BIOGL	biomphalari	
71	48	51.6	477	2	Q3YU3_BIOGL	biomphalari	
72	48	51.6	477	2	Q9K6M6_BACHD	bacillus ha	
73	47	50.5	687	2	Q6BM96_DEBHA	debaryomyce	
74	46.5	50.0	169	2	Q4DWK3_TRYCR	trypanosoma	
75	46	49.5	173	2	Q4E557_TRYCR	trypanosoma	
76	46	49.5	316	2	Q30RG4_THIDN	thiomicrosp	
77	46	49.5	467	2	Q5C081_SCHJA	schistosoma	
78	46	49.5	617	2	Q8XOM0_NEUCR	neurospora	
79	46	49.5	698	2	Q9USK4_SPOLT	spodoptera	
80	45.5	48.9	576	2	PTI_BUCBP	buchnera ap	
81	45	48.4	103	2	Q3YU3_BIOGL	biomphalari	
82	45	48.4	279	2	Q9K6M6_BACHD	bacillus ha	
83	45	48.4	344	2	Q4IBK7_GIBZE	gibberella	
84	45	48.4	546	2	Q4IR56_GIBZE	gibberella	
85	45	48.4	683	2	Q6J4Q1_APIME	apis mellif	
86	45	48.4	684	2	Q9GYW1_AEDAE	aedes aegyp	
87	45	48.4	684	2	Q9N2P8_DIPI	diploptera	
88	45	48.4	685	2	Q9GYW2_AEDAE	aedes aegyp	
89	45	48.4	114	2	Q4I728_GIBZE	gibberella	
90	44	47.3	227	2	Q3EGP5_ACTSC	actinobacil	
91	44	47.3	236	2	Q3VY94_9ACTO	actinobacil	
92	44	47.3	408	2	Q3CXS3_ALTAT	alteromonas	
93	44	47.3	498	2	Q7VQY1_BLOFL	blochmannia	
94	44	47.3	623	2	HCYE_EURCA	eurypelma c	
95	44	47.3	696	2	P02242_ANOGA	anopheles g	
96	44	47.3	696	2	Q7Q7X0_ANOGA	anopheles g	
97	44	47.3	704	1	SSP2_BOMMO	bombyx mori	
98	44	47.3	705	2	Q7PUR0_ANOGA	anopheles g	
99	44	47.3	738	2	Q44RM0_CHLLI	chlorobium	
100	44	47.3	1052	2	Q6MHO_DEBHA	debaryomyce	
101	43.5	46.8	214	2	Q9GKT8_MACFA	macaca fasc	
102	43.5	46.8	835	2	Q2K57_9REOV	human rotav	
103	43.5	46.8	1319	2	Q5RQ8_9EUKA	entamoeba h	
104	43	46.2	117	2	Q3V0M3_MOUSE	mus musculu	

Left block (rows 105–177)

#	Sc1	Sc2	Len	N	Accession	Organism
105	43	46.2	227	2	Q5PQ72_XENLA	xenopus lae
106	43	46.2	229	2	Q5BZA7_SCHJA	schistosoma
107	43	46.2	251	2	Q9ZKR7_HELPJ	helicobacte
108	43	46.2	308	2	Q8A2Q6_BACTN	bacteroides
109	43	46.2	320	2	Q58KH0_9BACT	leptospiril
110	43	46.2	344	2	Q8GEJ0_ERWPY	erwinia pyr
111	43	46.2	352	2	Q7M7X9_WOLSU	wolinella s
112	43	46.2	395	2	Q8X0K9_NEUCR	neurospora
113	43	46.2	500	2	Q7VG60_HELHP	helicobacte
114	43	46.2	578	2	Q61JE7_CAEBR	caenorhabdi
115	43	46.2	626	2	Q86N90_9ARAC	nephila ina
116	43	46.2	628	1	Q9NF14_ANOGA	anopheles g
117	43	46.2	632	2	Q7PXY7_ANOGA	anopheles g
118	43	46.2	638	2	HCYG_EURCA	europelma c
119	43	46.2	687	2	HCYG_EURCA	europelma c
120	43	46.2	689	2	Q58QB6_9TRYP	trypanosoma
121	43	46.2	690	2	P90664_AEDAE	aedes aegyp
122	43	46.2	690	2	Q22464_9GAMM	armigeres s
123	43	46.2	690	2	Q35UT4_9GAMM	shewanella
124	43	46.2	690	2	Q365G3_9GAMM	shewanella
125	43	46.2	690	2	Q3Q337_9GAMM	shewanella
126	43	46.2	690	2	Q8EFZ5_SHEON	shewanella
127	43	46.2	700	2	Q8EFZ5_SHEON	shewanella
128	43	46.2	700	2	Q7PI01_ANOGA	anopheles g
129	43	46.2	703	2	Q8MZM3_ANOGA	anopheles g
130	43	46.2	704	1	ARY_ANTPE	antheraea p
131	43	46.2	711	2	ARYB_MANSE	manduca sex
132	43	46.2	739	2	Q4P0X3_USTMA	ustilago ma
133	43	46.2	779	2	Q3VM70_9CHLB	pelodictyon
134	43	46.2	920	2	Q9KPM3_VIBCH	vibrio chol
135	43	46.2	1749	2	Q4T9T4_TETNG	tetraodon n
136	43	46.2	2238	2	Q7RGH9_PLAYO	plasmodium
137	43	46.2	186	2	Q54SY1_DICDI	dictyosteli
138	42.5	45.7	368	2	Q34VJ6_9GAMM	alkalilimni
139	42.5	45.7	395	2	Q86IM1_DICDI	dictyosteli
140	42.5	45.7	771	2	Q86IM1_DICDI	dictyosteli
141	42.5	45.7	1740	2	Q55923_DICDI	dictyosteli
142	42.5	45.2	162	2	Q4IJJ9_GIBZE	gibberella
143	42.5	45.2	211	1	Q6ENK5_ORYSA	oryza sativ
144	42.5	45.2	245	2	Q2WUV9_CLOBE	clostridium
145	42.5	45.2	318	2	Q89WK5_BRAJA	bradyrhizob
146	42.5	45.2	337	2	HAM1_BRAJA	candida alb
147	42.5	45.2	341	1	Q5A406_CANAL	synechococc
148	42.5	45.2	343	1	Q3AL39_SYNSC	drosophila
149	42.5	45.2	350	2	Q9GV29_DROME	haemophilus
150	42.5	45.2	351	2	MURB_HAEIN	chryseospir
151	42.5	45.2	351	2	P73784_SYNY3	burkholderi
152	42.5	45.2	351	2	Q42654_CHRAE	burkholderi
153	42.5	45.2	351	2	Q3F512_9BURK	burkholderi
154	42.5	45.2	385	2	Q44VD6_9BURK	burkholderi
155	42.5	45.2	394	2	Q4BPD2_BURVI	burkholderi
156	42.5	45.2	394	2	Q4BPD2_BURVI	vibrio fisc
157	42.5	45.2	418	1	Q4LXD0_9BURK	xylella fas
158	42.5	45.2	423	2	Q39FK9_BURS3	xylella fas
159	42.5	45.2	423	2	Q5ESP0_VIBFI	synechocyst
160	42.5	45.2	423	2	Q3QZP9_XYLFA	escherichia
161	42.5	45.2	423	2	Q3RDT1_XYLFA	escherichia
162	42.5	45.2	423	2	P73784_SYNY3	shigella bo
163	42.5	45.2	526	2	YHJV_ECOLI	shigella so
164	42.5	45.2	556	2	Q31V86_SHIBS	shigella fl
165	42.5	45.2	625	2	Q31VS0_SHISS	prochloroco
166	42.5	45.2	638	2	Q2M7K1_ECOLI	haloarcula
167	42.5	45.2	670	2	Q83PS2_SHIFL	nephila ina
168	42.5	45.2	685	2	Q7V2D6_PROMP	crocosphaer
169	42.5	45.2	685	2	Q5V0X8_HALMA	leptinotars
170	42.5	45.2	685	2	Q86N91_9ARAC	anopheles g
171	42.5	45.2	686	2	Q4CAY6_CROWT	anopheles g
172	42.5	45.2	686	2	Q5Z271_LEPDE	bombyx mori
173	42.5	45.2	686	2	Q7PPH1_ANOGA	anopheles g
174	42.5	45.2	687	2	Q8M2M2_ANOGA	anopheles g
175	42.5	45.2	687	2	Q9GU89_BOMMO	anopheles g
176	42.5	45.2	687	2	Q96753_ANOGA	anopheles g
177	42.5	45.2	690	2	Q27598_DROME	drosophila

Additional left-block accessions appearing in this range: Q44251_ANOGA, Q96453_ANOST, Q7PPF3_ANOGA, Q86RQ6_9DIPT, Q7P100_ANOGA.

Right block (rows 178–250)

#	Sc1	Sc2	Len	N	Accession	Organism
178	42	44.1	690	2	Q9V896_DROME	drosophila
179	42	44.1	749	2	Q4ANH6_9CHLB	chlorobium
180	45.2	44.1	751	2	Q4XU14_PLACH	plasmodium
181	45.2	44.1	751	2	Q7VNB0_HAEDU	haemophilus
182	45.2	44.1	831	2	Q9V706_DROME	drosophila
183	42	44.1	856	2	Q2Q2Q0_ORYSA	oryza sativ
184	42	44.1	909	2	Q7GIY6_ANOGA	anopheles g
185	45.2	44.1	1080	1	HDC_DROME	drosophila
186	42	44.1	1576	2	Q9N2M8_DROME	drosophila
187	41.5	44.1	92	2	Q3KN39_DROME	drosophila
188	42	44.6	173	2	Q3N6V2_9PROT	nitrosomona
189	41	44.1	125	2	Q7YVP8_9TRYP	trypanosoma
190	41	44.1	183	1	Q8CSR5_STAES	staphylococ
191	41	44.1	188	2	Q5F5T0_LEPIC	leptospira
192	41	44.1	194	2	Q8EXT3_LEPIN	leptospira
193	41	44.1	188	2	Q3CQ55_ALTAT	pseudoalter
194	41	44.1	194	2	Q5GJ05_PENJP	penaeus jap
195	41	44.1	195	2	Q82LN1_STRAW	streptomyce
196	41	44.1	213	2	Q4JVG7_CORJK	corynebacte
197	41	44.1	213	2	Q93MV1_9STRE	streptococc
198	41	44.1	229	2	Q9MC82_BPD3	bacteriopha
199	41	44.1	240	2	P06678_MAIZE	zea mays (m
200	41	44.1	241	2	Q946V7_MAIZE	zea mays (m
201	41	44.1	251	2	Q413H5_GIBZE	gibberella
202	41	44.1	253	2	Q3QGL2_9GAMM	shewanella
203	41	44.1	258	2	Q9VMS1_9PSED	pseudomonas
204	41	44.1	287	2	Q8VMS1_9PSED	pseudomonas
205	41	44.1	290	2	Q3QGI2_9GAMM	shewanella
206	41	44.1	296	2	Q5OR91_MOUSE	mus musculu
207	41	44.1	301	2	Q5SWU4_MOUSE	mus musculu
208	41	44.1	303	2	Q84X84_SOYBN	glycine max
209	41	44.1	308	2	Q84X83_SOYBN	glycine max
210	41	44.1	320	1	FAD3E_SOYBN	glycine max
211	41	44.1	341	2	Q5CD83_SOYBN	glycine max
212	41	44.1	355	2	P48625_SOYBN	glycine max
213	41	44.1	376	1	Q3ISH9_NATPD	natromonas
214	41	44.1	376	2	Q8KCE3_BACHD	bacillus ha
215	41	44.1	380	2	Q20629_ASPOR	aspergillus
216	41	44.1	380	2	Q96208_PLAF7	plasmodium
217	41	44.1	390	2	Q3VUR2_9CHLB	pelodictyon
218	41	44.1	427	2	Q44KV3_CHRSL	chromohalob
219	41	44.1	447	2	Q4WJE2_ASPFU	aspergillus
220	41	44.1	476	2	Q8MCQ3_9FABA	bradyrhizob
221	41	44.1	506	1	HCYB_PONLE	pontastacus
222	41	44.1	566	1	HCYA_CRRAE	carcinus ae
223	41	44.1	650	1	P84293_CARMA	carcinus ma
224	41	44.1	657	1	HCYA_PANIN	panulirus i
225	41	44.1	657	1	HCYE_PANIN	panulirus i
226	41	44.1	657	1	P10787_PANIN	panulirus i
227	41	44.1	659	1	P04254_CARMA	carcinus ma
228	41	44.1	662	2	Q7QE44_ANOGA	anopheles g
229	41	44.1	663	2	Q8IF58_9MYRI	scutigera c
230	41	44.1	669	1	HCYB_SCUCO	scutigera c
231	41	44.1	671	2	Q5G2A8_CANMG	cancer magi
232	41	44.1	675	2	Q5G2A7_CANMG	cancer magi
233	41	44.1	676	2	Q5G2A6_CANMG	cancer magi
234	41	44.1	676	2	Q9NFY6_PENVA	penaeus van
235	41	44.1	676	2	Q5G2A5_CANMG	cancer magi
236	41	44.1	680	2	Q23707_CANMG	cancer magi
237	41	44.1	684	2	Q5G2A4_CANMG	cancer magi
238	41	44.1	684	2	Q9NGL5_CALSI	callinectes
239	41	44.1	685	2	Q89UJ2_BRAJA	bradyrhizob
240	41	44.1	685	2	Q95P18_PALVU	palinurus v
241	41	44.1	685	2	Q95P19_PALVU	palinurus v
242	41	44.1	685	2	Q81FT5_EUCA	palinurus v
243	41	44.1	686	2	Q95P17_PALVU	palinurus v
244	41	44.1	687	2	Q5Y0Z1_PACLE	pacifastacu
245	41	44.1	688	2	Q4QAS4_LEIMA	leishmania
246	41	44.1	691	2	Q4GAS4_LEIMA	leishmania
247	41	44.1	744	2	Q9YOB3_SARBU	sarcophaga
248	41	44.1	750	2	Q6L466_SOLDE	solanum dem
249	41	44.1	753	2	Q9USY8_9HYME	camponotus
250	41	44.1	754	2	Q9Y1W5_TENMO	tenebrio mo

Additional right-block accessions appearing near the bottom: O77065_CHOFU (choristoneu).

OM protein - protein search, using sw model

GenCore version 5.1.9
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Run on: August 9, 2006, 15:36:13 ; Search time 39 Seconds
(without alignments)
41.941 Million cell updates/sec

Title: US-10-810-919-4
Perfect score: 93
Sequence: 1 VHHQKLPFFAEDVGSNK 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	84	90.8	42	2	PN0512	beta-amyloid prote
2	84	90.3	57	2	A60045	Alzheimer's diseas
3	84	90.3	57	2	F60045	Alzheimer's diseas
4	84	90.3	57	2	D60045	Alzheimer's diseas
5	84	90.3	57	2	B60045	Alzheimer's diseas
6	84	90.3	57	2	G60045	Alzheimer's diseas
7	84	90.3	57	2	C60045	Alzheimer's diseas
8	84	90.3	82	1	PQ0438	Alzheimer's diseas
9	84	90.3	695	1	A4979S	Alzheimer's diseas
10	84	90.3	770	1	QRHUA4	Alzheimer's diseas
11	80	86.0	770	2	JH0773	Alzheimer's diseas
12	80	86.0	33	2	S23094	beta-amyloid prote
13	76	81.7	695	2	A27485	Alzheimer's diseas
14	76	81.7	695	2	S00550	hypothetical prote
15	76	81.7	477	2	T47753	transcription regu
16	48	51.6	279	2	F84112	hypothetical prote
17	45	48.4	624	1	BHTLE	hemocyanin chain e
18	44	47.3	704	2	A34287	storage protein 2
19	44	47.3	251	2	C71879	hypothetical prote
20	43	46.2	703	2	B34434	arylphorin beta ch
21	43	46.2	779	2	A82089	hypothetical prote
22	43	46.2	341	2	G64058	UDP-N-acetylmurama
23	42	45.2	418	2	S74875	quinolone resistan
24	42	45.2	423	2	S47761	hypothetical 47.3K
25	42	45.2	649	2	S58064	hdc protein - frui
26	42	45.2	240	1	T2277S	19K zein precursor
27	41	44.1	259	2	ZIZMD1	hypothetical prote
28	41	44.1	320	2	C83628	probable oxidoredu
29	41	44.1	380	2	JQ2338	omega-3 fatty acid
30	41	44.1	390	2	D83853	cystathionine beta
31	41	44.1	447	2	D71611	hypothetical prote
32	41	44.1	657	1	BHL0A	hemocyanin chain a
33	41	44.1	657	1	BHL0B	hemocyanin chain b
34	40	43.0	220	2	AI2182	hypothetical prote
35	40	43.0	297	2	E56273	sapA 5'-region hyp
36	40	43.0	302	2	S37579	probable transposa
37	40	43.0	336	2	T38902	probable cinnamoyl
38	40	43.0	423	2	G86027	probable transport
39	40	43.0	423	2	C91181	probable histone d
40	40	43.0	491	2	D84967	glucose-6-phosphat
41	40	43.0	491	2	AB0742	glucose-6-phosphat
42	40	43.0	513	2	T01413	probable transport
43	40	43.0	626	2	S67964	hemocyanin chain 6
44	40	43.0	631	1	BHTLA	hemocyanin chain a
45	40	43.0	662	2	S55387	hemocyanin precurs
46	40	43.0	672	2	JC7676	hemocyanin A precu
47	40	43.0	699	2	H64118	4-alpha-glucanotra
48	40	43.0	702	2	CB6268	F13B4.2 protein -
49	40	43.0	992	1	GNWVR3	structural polypro
50	40	43.0	1063	1	GNWVR4	structural polypro
51	40	43.0	1063	1	GNWVRA	structural polypro
52	40	43.0	1063	1	S68430	structural polypro
53	39.5	42.5	493	1	G01932	queuine tRNA-ribos
54	39.5	42.5	494	2	D81140	queuine tRNA-ribos
55	39	41.9	292	2	D81880	probable 5,10-meth
56	39	41.9	292	2	F81880	probable 5,10-meth
57	39	41.9	313	2	C83874	arsenical pump-dri
58	39	41.9	334	2	JC4681	bradykinin B1 rece
59	39	41.9	357	2	T16256	hypothetical prote
60	39	41.9	382	2	T50426	hypothetical prote
61	39	41.9	394	2	T29813	F13B4.1 protein -
62	39	41.9	435	2	T37324	nicotinate phospho
63	39	41.9	435	2	AC0104	probable JNK-activ
64	39	41.9	448	2	A23690	probable sugar tra
65	39	41.9	455	2	B86268	3-chlorobenzoate-3
66	39	41.9	565	2	D82725	hemocyanin chain c
67	39	41.9	661	2	D82208	hemocyanin chain c
68	39	41.9	683	2	G86324	PIF1 protein homol
69	39	41.9	683	2	H90055	bifunctional beta-
70	39	41.9	723	1	G96795	hypothetical prote
71	39	41.9	900	1	AE1180	hypothetical prote
72	39	41.9	1299	2	AF1537	hypothetical prote
73	39	41.9	2374	1	C75103	transketolase (EC
74	38	40.9	202	2	A53901	malate synthase-re
75	38	40.9	273	2	B96663	conserved hypothet
76	38	40.9	311	2	C83304	hypothetical prote
77	38	40.9	319	2	T24415	hypothetical prote
78	38	40.9	354	2	T15824	hypothetical prote
79	38	40.9	367	2	A38926	glucan 1,6-alpha-i
80	38	40.9	390	1	B35387	glucose-6-phosphat
81	38	40.9	491	2	B82064	na+/h+ antiporter
82	38	40.9	535	1	S72438	B. subtilis YxjH a
83	38	40.9	641	2	B89793	B. subtilis YxjH a
84	38	40.9	667	2	A97174	protein kinase C (
85	38	40.9	682	2	A39666	organic solvent to
86	38	40.9	713	2	G69723	protein kinase C (
87	38	40.9	736	1	H97827	protein kinase C (
88	38	40.9	737	2	KIRBCE	protein kinase C (
89	38	40.9	737	2	KIMSCE	protein kinase C (
90	38	40.9	737	2	KIRTCE	ribonuclease P (EC
91	38	40.9	875	1	S28942	protein kinase C (
92	38	40.9	1026	2	A53901	hypothetical prote
93	38	40.9	1146	2	B96663	hypothetical prote
94	38	40.9	1231	2	C83304	hypothetical prote
95	38	40.9	1238	2	T24415	hypothetical prote
96	38	40.9	1377	2	T15824	DNA-binding protei
97	38	40.9	1377	2	A38926	hypothetical prote
98	37.5	40.3	225	2	B35387	fructose-1,6-bisph
99	37.5	40.3	336	2	B82064	hypothetical prote
100	37.5	40.3	409	2	S72438	phosphatidylserine
101	37	39.8	130	2	B89793	hypothetical prote
102	37	39.8	166	2	A97174	chemotaxis protein

No			Len	N	Accession	Description
103	37	39.8	173	2	D86825	pyrimidine operon
104	37	39.8	175	2	A99892	pyrimidine operon
105	37	39.8	175	2	F82486	conserved hypothet
106	37	39.8	178	2	D97160	uracil phosphoribo
107	37	39.8	178	1	G64069	uracil phosphoribo
108	37	39.8	179	1	S38892	uracil phosphoribo
109	37	39.8	183	2	E75435	pyrimidine operon
110	37	39.8	183	2	AH1304	pyrimidine operon
111	37	39.8	183	2	AH1676	pyrimidine operon
112	37	39.8	183	2	H87707	alkyl hydroperoxid
113	37	39.8	193	2	H70958	probable uracil ph
114	37	39.8	199	2	S26047	transformer sex-de
115	37	39.8	240	2	C87409	hypothetical prote
116	37	39.8	247	2	H69827	conserved hypothet
117	37	39.8	255	2	S41511	Brn-3a protein - m
118	37	39.8	263	2	I40199	transposase - Bact
119	37	39.8	276	2	C64417	hypothetical prote
120	37	39.8	296	2	I46021	Fc-gamma receptor
121	37	39.8	301	2	PQ0162	arylphorin (clone
122	37	39.8	306	2	G69674	beta-lactamase (EC
123	37	39.8	349	2	T31788	hypothetical prote
124	37	39.8	351	2	S76925	hypothetical prote
125	37	39.8	371	2	AH0686	hypothetical prote
126	37	39.8	381	2	P84107	glycosyltransferas
127	37	39.8	387	2	G70398	1,3 propanediol de
128	37	39.8	419	1	T00425	erythromycin ester
129	37	39.8	424	1	E69659	tyrosine-tRNA liga
130	37	39.8	430	1	B80289	molybdopterin bios
131	37	39.8	447	2	AC1926	photolyase/blue-li
132	37	39.8	475	2	E70363	hypothetical prote
133	37	39.8	485	2	A80252	4-alpha-glucanotra
134	37	39.8	494	2	AH0289	glucose-6-phosphat
135	37	39.8	499	2	E82977	4-alpha-glucanotra
136	37	39.8	502	2	E71963	glyoxylate oxidase
137	37	39.8	502	2	F64543	probable cardioli
138	37	39.8	533	2	S43142	conserved hypothet
139	37	39.8	537	2	AE2454	sucrose transport
140	37	39.8	548	2	S37969	two-component sens
141	37	39.8	632	2	I51682	probable triacylgl
142	37	39.8	687	2	JQ1044	epithelial sodium
143	37	39.8	748	2	B45046	arylphorin precurs
144	37	39.8	759	2	JQ1045	arylphorin precurs
145	37	39.8	762	2	H71916	basic juvenile hor
146	37	39.8	832	2	H84848	DNA mismatch repai
147	37	39.8	1341	2	AE2454	phospholipase D [i
148	37	39.8	1341	2	T18301	latrophilin-2, spl
149	37	39.8	1354	2	T18375	latrophilin-2, spl
150	37	39.8	1356	2	T18367	latrophilin-2, spl
151	37	39.8	1369	2	T18379	latrophilin-2, spl
152	37	39.8	1375	2	T30813	latrophilin-2, spl
153	37	39.8	1384	2	T18366	plasminogen relate
154	37	39.8	1397	2	T18377	latrophilin-2, spl
155	37	39.8	1399	2	T18370	latrophilin-2, spl
156	37	39.8	1407	2	T18381	latrophilin-2, spl
157	37	39.8	1412	2	T18380	latrophilin-2, spl
158	37	39.8	1420	2	T18385	latrophilin-2, spl
159	37	39.8	1422	2	T18383	latrophilin-2, spl
160	37	39.8	1435	2	T18387	latrophilin-2, spl
161	37	39.8	1450	2	T18382	latrophilin-2, spl
162	37	39.8	1463	2	T18386	latrophilin-2, spl
163	37	39.8	1465	2	T18384	latrophilin-2, spl
164	37	39.8	1478	2	T18388	latrophilin-2, spl
165	37	39.8	2150	1	S27802	zinc finger protei
166	37	39.8	2150	2	T19450	hypothetical prote
167	37	39.8	3135	2	A48584	histatin 1 precurs
168	36.5	39.2	57	2	A32541	nucleoside-diphosp
169	36.5	39.2	153	2	JC8359	transmission block
170	36.5	39.2	195	2	A99240	anthranilate synth
171	36.5	39.2	195	2	B40635	anthranilate synth
172	36.5	39.2	284	2	A12008	formyltetrahydrofo
173	36.5	39.2	297	2	AF1618	endonuclease IV ho
174	36.5	39.2	371	2	T08485	klcB protein - Ent
175	36.5	39.2	551	2	P70111	V-type ATPase, sub
176	36.5	39.2	2628	2	S59413	probable membrane
177	36	38.7	98	2	A89892	S-100 calcium-bind
178	36	38.7	98	2	JC5064	calcium-binding pr
179	36	38.7	109	2	JC5065	hypothetical prote
180	36	38.7	134	2	C64402	calcium-binding pr
181	36	38.7	142	2	F64861	ycgX protein - Esc
182	36	38.7	151	2	T45922	probable C2H2-type
183	36	38.7	179	2	A86695	hypothetical prote
184	36	38.7	181	2	G87439	conserved hypothet
185	36	38.7	181	2	B57986	uracil phosphoribo
186	36	38.7	225	2	C70045	two-component resp
187	36	38.7	236	2	AG3072	conserved hypothet
188	36	38.7	236	2	B98214	bbsI protein (AF17
189	36	38.7	245	2	JE0179	protein-glutamine
190	36	38.7	255	1	T22863	hypothetical prote
191	36	38.7	276	1	BVECGG	gipG protein - Esc
192	36	38.7	276	2	D86008	protein of gip reg
193	36	38.7	284	2	C91162	protein of gip reg
194	36	38.7	289	2	C83237	probable transcrip
195	36	38.7	308	2	E64330	dihydrodipicolinat
196	36	38.7	312	2	D81297	probable selenide,
197	36	38.7	315	2	T27004	hypothetical prote
198	36	38.7	331	2	F90589	conserved hypothet
199	36	38.7	342	2	E83368	two-component resp
200	36	38.7	348	2	AF1203	transcription regu
201	36	38.7	348	2	T13320	hypothetical prote
202	36	38.7	360	2	T13625	hypothetical prote
203	36	38.7	362	2	AF0159	nuclear hormone re
204	36	38.7	365	2	C64309	two-component sens
205	36	38.7	368	2	A11934	zinc-finger protei
206	36	38.7	371	2	B84714	response regulator
207	36	38.7	378	2	B84113	probable ARP2/3 pr
208	36	38.7	378	2	B84719	probable ARP2/3 pr
209	36	38.7	400	2	D64462	hypothetical prote
210	36	38.7	420	2	C87790	protein B0207.3 [i
211	36	38.7	434	2	T04471	probable 4-hydroxy
212	36	38.7	453	2	A55212	anthranilate synth
213	36	38.7	456	2	B96688	unknown protein, 1
214	36	38.7	458	2	C82952	hypothetical prote
215	36	38.7	458	2	T33814	ATP synthase beta
216	36	38.7	467	2	S61105	hypothetical prote
217	36	38.7	486	2	E87566	hypothetical prote
218	36	38.7	487	2	C98076	hypothetical prote
219	36	38.7	491	2	D64947	hypothetical prote
220	36	38.7	491	1	F85797	anthranilate synth
221	36	38.7	491	1	B90949	hypothetical prote
222	36	38.7	491	2	B96691	hypothetical prote
223	36	38.7	492	2	A84520	probable sucrose-p
224	36	38.7	499	2	S74396	probable sucrose-p
225	36	38.7	499	2	C70405	probable membrane
226	36	38.7	503	2	A12342	probable sucrose-p
227	36	38.7	523	2	T40370	hypothetical prote
228	36	38.7	527	2	T22867	hypothetical prote
229	36	38.7	550	2	A48026	sterol O-acyltrans
230	36	38.7	580	2	T40867	aspartate-tRNA lig
231	36	38.7	586	2	S66697	probable membrane
232	36	38.7	592	2	H69430	Na+ channel protei
233	36	38.7	669	2	A44434	sodium channel pro
234	36	38.7	669	2	S29499	arylphorin alpha c
235	36	38.7	699	2	A49585	probable receptor
236	36	38.7	702	2	T15413	probable formate C
237	36	38.7	776	2	TO1547	probable phospholi
238	36	38.7	833	2	SS0801	AMP deaminase homo
239	36	38.7	888	2	SS0784	FAbI protein homol
240	36	38.7	990	2	TO3784	laminin alpha-2 ch
241	36	38.7	1236	1	B36329	hypothetical prote
242	36	38.7	1314	1	TNBYR6	transcription regu
243	36	38.7	1375	2	T18961	hypothetical prote
244	36	38.7	1375	1	MHIUMH	probable receptor
245	36	38.7	1751	1	T19821	hypothetical prote
246	36	38.7	3775	2	S09752	probable phospholi
247	35.5	38.2	114	2	F81350	hypothetical prote
248	35.5	38.2	274	2		formyltetrahydrofo

OM protein - protein search, using sw model

GenCore version 5.1.9
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Run on: August 9, 2006, 15:31:47 ; Search time 194 Seconds
                                            (without alignment)
                                            40.065 Million cell updates/sec

Title: US-10-810-919-4
Perfect score: 93
Sequence: 1 VHHQKLPFFAEDVGSNK 17

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 45721629 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :   A.geneseqp.8:*
                1: geneseqp1980s:*
                2: geneseqp1990s:*
                3: geneseqp2000s:*
                4: geneseqp2001s:*
                5: geneseqp2002s:*
                6: geneseqp2003as:*
                7: geneseqp2003bs:*
                8: geneseqp2004s:*
                9: geneseqp2005s:*
                10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	93	100.0	17	8	ADS18448	Ads18448 Amyloid-b
2	84	90.3	17	2	AAR54703	Aar54703 Beta-amyl
3	84	90.3	17	4	AAB91774	Aab91774 Amyloid b
4	84	90.3	17	9	AAB91807	Aab91807 Amyloid b
5	84	90.3	17	5	ABB04911	Abb04911 Human amy
6	84	90.3	17	6	ABB99611	Abb99611 Peptide d
7	84	90.3	17	9	ADG93165	Adg93165 Novel exp
8	84	90.3	17	8	ADJ65843	Adj65843 Amyloid B
9	84	90.3	17	8	ADN02827	Adn02827 Mammalian
10	84	90.3	17	8	ADS18447	Ads18447 Amyloid-b
11	84	90.3	18	3	AAB10963	Aab10963 Beta-amyl
12	84	90.3	18	3	ADW88085	Adw88085 T668 phos
13	84	90.3	24	9	AEB09194	Aeb09194 Human bet
14	84	90.3	24	9	AED47504	Aed47504 Linker pe
15	84	90.3	26	2	AAW47229	Aaw47229 Human amy
16	84	90.3	26	2	AAY33408	Aay33408 Human amy
17	84	90.3	26	9	ADY72250	Ady72250 N-termina
18	84	90.3	27	4	ADY33409	Ady33409 Human amy
19	84	90.3	28	1	AAP70594	Aap70594 Sequence
20	84	90.3	28	2	AAR60368	Aar60368 Beta-amyl
21	84	90.3	28	2	AAR54702	Aar54702 Beta-amyl
22	84	90.3	28	2	AAR64171	Aar64171 A4-P(1-28
23	84	90.3	28	2	AAR64172	Aar64172 A4-B(1-28
24	84	90.3	28	2	AAW01413	Aaw01413 Beta/A4-a
25	84	90.3	28	2	AAY39805	Aay39805 Beta-amyl
26	84	90.3	28	2	AAW81467	Aaw81467 Synthetic
27	84	90.3	28	4	AAB35591	Aab35591 Human clo
28	84	90.3	28	4	AAB35595	Aab35595 Human clo
29	84	90.3	28	4	AAB35594	Aab35594 Human clo
30	84	90.3	28	4	AAB35592	Aab35592 Human clo
31	84	90.3	28	4	AAB35593	Aab35593 Human clo
32	84	90.3	28	4	AAB35596	Aab35596 Human clo
33	84	90.3	28	4	AAB35590	Aab35590 Human clo
34	84	90.3	28	4	AAB91816	Aab91816 Amyloid b
35	84	90.3	28	4	AAB91789	Aab91789 Amyloid b
36	84	90.3	28	4	AAB91827	Aab91827 Amyloid b
37	84	90.3	28	4	AAB91783	Aab91783 Amyloid b
38	84	90.3	28	4	AAB91800	Aab91800 Amyloid b
39	84	90.3	28	4	AAB49396	Aab49396 Human amy
40	84	90.3	28	5	AAE21439	Aae21439 Human amy
41	84	90.3	28	5	ABB76030	Abb76030 Beta amyl
42	84	90.3	28	5	AAO18476	Aao18476 Human bet
43	84	90.3	28	5	AAU76484	Aau76484 Amino aci
44	84	90.3	28	5	ABB04910	Abb04910 Human amy
45	84	90.3	28	5	AAE26081	Aae26081 Beta amyl
46	84	90.3	28	5	AAM50910	Aam50910 Beta amyl
47	84	90.3	28	5	ABB77991	Abb77991 Fragment
48	84	90.3	28	6	AAE35672	Aae35672 Human bet
49	84	90.3	28	6	AAE33794	Aae33794 Beta-amyl
50	84	90.3	28	6	ABG72238	Abg72238 Mutant H6
51	84	90.3	28	6	ABG72234	Abg72234 Wild-type
52	84	90.3	28	6	ABG72235	Abg72235 Mutant D1
53	84	90.3	28	6	ABG72240	Abg72240 Mutant E1
54	84	90.3	28	6	ABG72237	Abg72237 Mutant R5
55	84	90.3	28	6	ABG72236	Abg72236 Mutant E3
56	84	90.3	28	6	ABG72239	Abg72239 Mutant D7
57	84	90.3	28	6	AAE35431	Aae35431 Abeta pep
58	84	90.3	28	6	AAE33219	Aae33219 Beta amyl
59	84	90.3	28	6	ABU63712	Abu63712 Rat amylo
60	84	90.3	28	7	AAE38831	Aae38831 Membrane
61	84	90.3	28	8	ADF55641	Adf55641 Human A b
62	84	90.3	28	8	ADO04475	Ado04475 Beta-amyl
63	84	90.3	28	8	ADQ37255	Adq37255 Vaccine a
64	84	90.3	28	8	ADR16886	Adr16886 A disinte
65	84	90.3	28	8	ADS15333	Ads15333 Beta-amyl
66	84	90.3	28	9	ADY81768	Ady81768 Human bet
67	84	90.3	28	9	AEC39345	Aec39345 Amyloid b
68	84	90.3	28	9	AED47507	Aed47507 Inhibitor
69	84	90.3	28	9	AED47505	Aed47505 Inhibitor
70	84	90.3	29	5	AAE26331	Aae26331 Human bet
71	84	90.3	29	9	ADW88083	Adw88083 T668 phos
72	84	90.3	30	2	AAW81468	Aaw81468 Synthetic
73	84	90.3	30	5	AAU11766	Aau11766 Human amy
74	84	90.3	30	7	ABR42769	Abr42769 Human amy
75	84	90.3	30	7	ADK82701	Adk82701 Beta-amyl
76	84	90.3	30	8	ADI35870	Adi35870 Amyloid b
77	84	90.3	30	9	ADZ59196	Adz59196 Human amy
78	84	90.3	32	4	AAB84430	Aab84430 Partial s
79	84	90.3	32	9	ADP73486	Adp73486 Alzheimer
80	84	90.3	32	9	AED47511	Aed47511 Beta secr
81	84	90.3	33	2	AAW81469	Aaw81469 Synthetic
82	84	90.3	33	3	AAU93990	Aau93990 Human bet
83	84	90.3	33	7	ADE10851	Ade10851 Chimeric
84	84	90.3	33	7	ADG63951	Adg63951 Recombina
85	84	90.3	33	8	ADP73485	Adp73485 Alzheimer
86	84	90.3	33	8	ADR12778	Adr12778 Human bet
87	84	90.3	35	2	AAW47228	Aaw47228 Beta-amyl
88	84	90.3	35	2	AAW89361	Aaw89361 Beta-amyl
89	84	90.3	35	2	AAW89357	Aaw89357 Beta-amyl
90	84	90.3	35	8	ADQ37254	Adq37254 Vaccine
91	84	90.3	35	8	AAE35430	Aae35430 Abeta pep
92	84	90.3	36	2	AAW81471	Aaw81471 Beta-amyl
93	84	90.3	36	6	AAU11776	Aau11776 Synthetic
94	84	90.3	36	5	AAU11771	Aau11771 Synthetic
95	84	90.3	36	6	AAE35430	Aae35430 Vaccine
96	84	90.3	36	6	ABR42779	Abr42779 Amyloid b

Seq	Len	Score	C1	C2	Code	Description
97	84	90.3	36	6	ABR42774	Abr42774 Amyloid b
98	84	90.3	36	8	ADP73823	Adp73823 Loop inse
99	84	90.3	36	8	AED47512	Aed47512 Beta secr
100	84	90.3	36	10	AEE39871	Aee39871 Amyloidge
101	84	90.3	38	2	AAR60362	Aar60362 Beta-amyl
102	84	90.3	38	4	AAW92722	Aaw92722 Human tac
103	84	90.3	38	4	AAB91826	Aab91826 Amyloid b
104	84	90.3	38	4	AAB91799	Aab91799 Amyloid b
105	84	90.3	38	4	ADU24436	Adu24436 Novel glu
106	84	90.3	38	8	ADU24441	Adu24441 Novel glu
107	84	90.3	38	8	ADU46715	Adu46715 Gln3 amyl
108	84	90.3	38	8	ADU46710	Adu46710 Amyloid b
109	84	90.3	38	8	ADY81762	Ady81762 Human bet
110	84	90.3	38	8	ADZ71362	Adz71362 Human bet
111	84	90.3	38	9	ADZ71367	Adz71367 Human bet
112	84	90.3	38	9	AEA35400	Aea35400 Novel QC
113	84	90.3	38	9	AEA35395	Aea35395 Novel QC
114	84	90.3	38	9	AEB92568	Aeb92568 Glutamin
115	84	90.3	38	10	AEB92573	Aeb92573 Glutamin
116	84	90.3	38	10	AEE39872	Aee39872 Amyloidge
117	84	90.3	39	9	ADY81763	Ady81763 Human bet
118	84	90.3	39	9	ABP96148	Abp96148 Human Abe
119	84	90.3	39	2	AAW81472	Aaw81472 Synthetic
120	84	90.3	39	2	AAR60363	Aar60363 Beta-amyl
121	84	90.3	39	2	AAY25134	Aay25134 Human amy
122	84	90.3	39	2	AAY52132	Aay52132 Human Rec
123	84	90.3	39	6	ABU08509	Abu08509 Amyloid b
124	84	90.3	39	10	AEF87774	Aef87774 Human amy
125	84	90.3	40	2	AAR33191	Aar33191 Beta-amyl
126	84	90.3	40	2	AAR60364	Aar60364 Beta-amyl
127	84	90.3	40	2	ADD11651	Add11651 Human bet
128	84	90.3	40	2	AAW23335	Aaw23335 Amyloid b
129	84	90.3	40	4	AAW37507	Aaw37507 Amyloid b
130	84	90.3	40	4	AAW47226	Aaw47226 Amyloid b
131	84	90.3	40	4	AAY14099	Aay14099 Human bet
132	84	90.3	40	4	AAY39804	Aay39804 Beta-amyl
133	84	90.3	40	4	AAW95584	Aaw95584 Wild type
134	84	90.3	40	2	AAW81473	Aaw81473 Synthetic
135	84	90.3	40	2	AAY39939	Aay39939 Beta-amyl
136	84	90.3	40	2	AAY25135	Aay25135 Human amy
137	84	90.3	40	2	AAW92723	Aaw92723 Human tac
138	84	90.3	40	2	AAB84426	Aab84426 Partial B
139	84	90.3	40	4	AAB84429	Aab84429 Partial s
140	84	90.3	40	4	AAB91813	Aab91813 Amyloid b
141	84	90.3	40	4	AAB91780	Aab91780 Amyloid b
142	84	90.3	40	4	AAB91829	Aab91829 Amyloid b
143	84	90.3	40	4	AAB91802	Aab91802 Amyloid b
144	84	90.3	40	4	AAE05483	Aae05483 Human pep
145	84	90.3	40	5	AAU99425	Aau99425 Human amy
146	84	90.3	40	5	AAE22990	Aae22990 Human amy
147	84	90.3	40	5	AAU11773	Aau11773 Synthetic
148	84	90.3	40	5	AAU11772	Aau11772 Synthetic
149	84	90.3	40	5	AAG68313	Aag68313 Human sel
150	84	90.3	40	5	AAU96895	Aau96895 Human sel
151	84	90.3	40	5	AAM50909	Aam50909 Beta amyl
152	84	90.3	40	5	AAU80186	Aau80186 Human bet
153	84	90.3	40	5	AAE26332	Aae26332 Human bet
154	84	90.3	40	5	AAM51863	Aam51863 Human bet
155	84	90.3	40	6	ABU08710	Abu08710 Amyloid b
156	84	90.3	40	6	ABU08508	Abu08508 Human amy
157	84	90.3	40	6	AAO19885	Aao19885 Human amy
158	84	90.3	40	6	ABP96147	Abp96147 Human Abe
159	84	90.3	40	6	AAE35429	Aae35429 Abeta pro
160	84	90.3	40	6	ABP60626	Abp60626 Human A-b
161	84	90.3	40	6	ABP97883	Abp97883 Amino aci
162	84	90.3	40	6	ABR42775	Abr42775 Amyloid b
163	84	90.3	40	6	ABR42776	Abr42776 Amyloid b
164	84	90.3	40	6	ABU63706	Abu63706 Rat amylo
165	84	90.3	40	6	ADA37266	Ada37266 Human bet
166	84	90.3	40	7	ADB85563	Adb85563 Beta-amyl
167	84	90.3	40	7	AAE38648	Aae38648 Human A/b
168	84	90.3	40	7	ADC66001	Adc66001 Human amy
169	84	90.3	40	7	ADC35182	Adc35182 Beta-amyl
170	84	90.3	40	7	ADF55648	Adf55648 Human A b
171	84	90.3	40	7	ADK82702	Adk82702 Beta-amyl
172	84	90.3	40	8	ADF53270	Adf53270 Amyloid A
173	84	90.3	40	8	ADN00693	Adn00693 A40, SEQ
174	84	90.3	40	8	ADN41885	Adn41885 Amino aci
175	84	90.3	40	8	ADN41881	Adn41881 Amino aci
176	84	90.3	40	8	ADN41882	Adn41882 Amino aci
177	84	90.3	40	8	ADN41884	Adn41884 Amino aci
178	84	90.3	40	8	ADN41865	Adn41865 Amino aci
179	84	90.3	40	8	ADN41880	Adn41880 Amino aci
180	84	90.3	40	8	ADO10000	Ado10000 Human amy
181	84	90.3	40	8	ADQ26239	Adq26239 Human amy
182	84	90.3	40	8	ADQ37253	Adq37253 Human bet
183	84	90.3	40	8	ADR16410	Adr16410 Human Abe
184	84	90.3	40	8	ADS18445	Ads18445 Amyloid-b
185	84	90.3	40	8	ADU20812	Adu20812 Novel QC
186	84	90.3	40	8	ADU24435	Adu24435 Novel glu
187	84	90.3	40	8	ADU24434	Adu24434 Novel glu
188	84	90.3	40	8	ADZ20480	Adz20480 Amyloid b
189	84	90.3	40	8	ADV50991	Adv50991 Alzheimer
190	84	90.3	40	8	ADW38388	Adw38388 Human bet
191	84	90.3	40	9	ADY72249	Ady72249 N-termina
192	84	90.3	40	9	ADY81764	Ady81764 Human bet
193	84	90.3	40	9	ADY78385	Ady78385 Human bet
194	84	90.3	40	9	AEB88137	Aeb88137 Human nep
195	84	90.3	40	9	AEB92566	Aeb92566 Glutamin
196	84	90.3	40	9	AEC05253	Aec05253 Amyloid b
197	84	90.3	40	9	AEC39344	Aec39344 Amyloid b
198	84	90.3	40	9	AED21140	Aed21140 Amyloid b
199	84	90.3	40	9	AEA35394	Aea35394 Novel QC
200	84	90.3	40	9	AEA35393	Aea35393 Novel QC
201	84	90.3	40	9	AEB09193	Aeb09193 Human bet
202	84	90.3	40	9	AEB92567	Aeb92567 Glutamin
203	84	90.3	40	9	AEB92566	Aeb92566 Glutamin
204	84	90.3	40	9	AEC05253	Aec05253 Amyloid b
205	84	90.3	40	9	AEC39344	Aec39344 Amyloid b
206	84	90.3	40	9	AED21140	Aed21140 Amyloid b
207	84	90.3	40	9	AED26003	Aed26003 Human amy
208	84	90.3	40	9	AED83058	Aed83058 Human amy
209	84	90.3	40	9	AEE83386	Aee83386 Amyloid b
210	84	90.3	40	10	AEF92526	Aef92526 Human amy
211	84	90.3	40	10	AEF87773	Aef87773 Human amy
212	84	90.3	41	2	AEF83486	Aef83486 Amyloid b
213	84	90.3	41	2	AAR60365	Aar60365 Beta-amyl
214	84	90.3	41	2	AAR65283	Aar65283 Beta amyl
215	84	90.3	41	3	AAY25136	Aay25136 Human amy
216	84	90.3	41	6	AAB11497	Aab11497 Human amy
217	84	90.3	41	6	ABU08507	Abu08507 Human amy
218	84	90.3	41	6	ABP96146	Abp96146 Human Abe
219	84	90.3	41	9	ADN41883	Adn41883 Amino aci
220	84	90.3	41	9	ADY81765	Ady81765 Human bet
221	84	90.3	42	2	AAR20030	Aar20030 Sequence
222	84	90.3	42	2	AAR60366	Aar60366 Beta-amyl
223	84	90.3	42	2	AAR65287	Aar65287 Beta amyl
224	84	90.3	42	2	AAR65288	Aar65288 Beta amyl
225	84	90.3	42	2	AAR65285	Aar65285 Beta amyl
226	84	90.3	42	2	AAR65286	Aar65286 Beta amyl
227	84	90.3	42	2	AAR95248	Aar95248 Beta/A4-a
228	84	90.3	42	2	AAR94591	Aar94591 Beta/A4-a
229	84	90.3	42	2	AAW12828	Aaw12828 Human amy
230	84	90.3	42	2	AAW64507	Aaw64507 Amyloid b
231	84	90.3	42	2	AAW42989	Aaw42989 Human Abe
232	84	90.3	42	2	AAW47230	Aaw47230 Neurotoxi
233	84	90.3	42	2	AAY49691	Aay49691 Amyloid b
234	84	90.3	42	2	AAW99585	Aaw99585 Beta A4 P
235	84	90.3	42	2	AAW81474	Aaw81474 Alzheimer
236	84	90.3	42	2	AAY08607	Aay08607 Beta amyl
237	84	90.3	42	2	AAW29093	Aaw29093 A-beta-bi
238	84	90.3	42	2	AAY25137	Aay25137 Human amy
239	84	90.3	42	2	AAY29093	Aay29093 Human amy
240	84	90.3	42	2	AAW92726	Aaw92726 Human tac
241	84	90.3	42	3	AAY33407	Aay33407 Beta-amyl
242	84	90.3	42	4	AAY96956	Aay96956 Beta-amyl